



Conseiller.ST25
SUBSTITUTE SEQUENCE LISTING

<110> Conseiller, Emmanuel
Debussche, Laurent
Gallagher, William

<120> Polypeptide (MBP1) Capable Of Interacting With Oncogenic Mutants Of The P53 Protein

<130> ST98033

<140> 09/829,936

<141> 2001-04-11

<150> FR9812754

<151> 1998-10-12

<160> 35

<170> PatentIn version 3.3

<210> 1

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5'-1(p53)

<400> 1

agatctgtat ggaggagccg cag

23

<210> 2

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' -393 (p53)

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<400> 2
agatctcatc agtctgagtc aggcccttc

29

<210> 3

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide H175 3'

<400> 3
ggggcagtgc ctcac

15

<210> 4

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide w248 3'

<400> 4
gggcctccag ttcac

15

<210> 5

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide H273 3'

<400> 5
acaaacatgc acctc

15

<210> 6

<211> 15

<212> DNA

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<213> Artificial Sequence

<220>

<223> oligonucleotide G281 3'

<400> 6

gcgccggcct ctccc

15

<210> 7

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5'-73

<400> 7

agatctgtgt ggcccctgca cca

23

<210> 8

<211> 1021

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 8

tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg gac
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

48

ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac ctg
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

96

ccg ggc tcc ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga cct
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

144

aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc cca
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

192

tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgt
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys

240

65	Conseiller.ST25										80														
	70	75																							
aac Asn	cag Gln	ggc Gly	tat Tyr	gag Glu 85	ctg Leu	cac His	cgg Arg	gat Asp	ggc Gly 90	ttc Phe	tcc Ser	tgc Cys	agc Ser 95	gat Asp	atc Ile	288									
gat Asp	gag Glu	tgc Cys	ggc Gly 100	tac Tyr	tcc Ser	agt Ser	tac Tyr	ctc Leu 105	tgc Cys	cag Gln	tac Tyr	cgc Arg	tgt Cys 110	gtc Val	aac Asn	336									
gag Glu	cca Pro	ggc Gly 115	cga Arg	ttc Phe	tcc Ser	tgt Cys	cac His 120	tgc Cys	cca Pro	caa Gln	ggc Gly 125	tac Tyr	cag Gln	ctg Leu	ctg Leu	384									
gct Ala 130	aca Thr	agg Arg	ctc Leu	tgc Cys	caa Gln	gat Asp 135	att Ile	gac Asp	gag Glu	tgt Cys	gaa Glu 140	aca Thr	ggt Gly	gca Ala	cac His	432									
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tca Ser	tcc Ser	att Ile 195	gtg Val	cac His	cgc Arg	tac Tyr	atg Met 200	agc Ser	atc Ile	acc Thr	tca Ser	gag Glu 205	cga Arg	agt Ser	gtg Val	624									
cct Pro 210	gct Ala	gac Asp	gtg Val	ttt Phe	cag Gln	atc Ile 215	cag Gln	gca Ala	acc Thr	tct Ser	gtc Val 220	tac Tyr	cct Pro	ggt Gly	gcc Ala	672									
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att Ile	agg Arg	caa Gln	atc Ile	aac Asn 245	aat Asn	gtc Val	agc Ser	gcc Ala	atg Met 250	ctg Leu	gtc Val	ctc Leu	gcc Ala	agg Arg 255	cca Pro	768									
gtg Val	acg Thr	gga Gly	ccc Pro 260	cgg Arg	gag Glu	tac Tyr	gtg Val	ctg Leu 265	gac Asp	ctg Leu	gag Glu	atg Met	gtc Val 270	acc Thr	atg Met	816									
aat Asn	tcc Ser	ctt Leu 275	atg Met	agc Ser	tac Tyr	cgg Arg	gcc Ala 280	agc Ser	tct Ser	gta Val	ctg Leu	aga Arg	ctc Leu	acg Thr	gtc Val	864									
ttt Phe 290	gtg Val	gga Gly	gcc Ala	tat Tyr	acc Thr	ttc Phe 295	tgaagaccct caggggaaggg ccatgtgggg									915									
gccccttccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt																975									
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<210> 9

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine MBP1 C-term fragment

<400> 9

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala His
130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser Asp
165 170 175

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

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Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 10

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide c-myc 5'

<400> 10

gatccatgga gcagaagctg atctccgagg aggacctga

39

<210> 11

<211> 39

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide c-myc 3'

<400> 11

gatctcaggt cctcctcgga gatacagcttc tgctccatg

39

<210> 12

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<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' MCS oligonucleotide

<400> 12

gatctcgggc gacctgcatg caattcccgg gtgcggccgc gagct

45

<210> 13

<211> 37

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' MCS oligonucleotide

<400> 13

cgcggccgca cccgggaatt gcatgcaggt cgaccga

37

<210> 14

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' mMBP1

<400> 14

cggtactggc agaggtaact gg

22

<210> 15

<211> 1513

<212> DNA

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<220>

<221> CDS

<222> (49)..(1377)

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<400> 15

gctgtggcag aaacccctga cttctgcca ccacctcca gcctcagg atg ctc cct 57
Met Leu Pro
1

ttt gcc tcc tgc ctc ccc ggg tct ttg ctg ctc tgg gcg ttt ctg ctg 105
Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala Phe Leu Leu
5 10 15

ttg ctc ttg gga gca gcg tcc cca cag gat ccc gag gag ccg gac agc 153
Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu Pro Asp Ser
20 25 30 35

tac acg gaa tgc aca gat ggc tat gag tgg gat gca gac agc cag cac 201
Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp Ser Gln His
40 45 50

tgc cgg gat gtc aac gag tgc ctg acc atc ccg gag gct tgc aag ggt 249
Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala Cys Lys Gly
55 60 65

gag atg aaa tgc atc aac cac tac ggg ggt tat ttg tgt ctg cct cgc 297
Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys Leu Pro Arg
70 75 80

tct gct gcc gtc atc agt gat ctc cat ggt gaa gga cct cca ccg cca 345
Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro Pro Pro Pro
85 90 95

gcg gcc cat gct caa caa cca aac cct tgc ccg cag ggc tac gag cct 393
Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly Tyr Glu Pro
100 105 110 115

gat gaa cag gag agc tgt gtg gat gtg gac gag tgt acc cag gct ttg 441
Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr Gln Ala Leu
120 125 130

cat gac tgt cgc cct agt cag gac tgc cat aac ctt cct ggc tcc tac 489
His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro Gly Ser Tyr
135 140 145

cag tgc acc tgc cct gat ggt tac cga aaa att gga ccc gaa tgt gtg 537
Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val
150 155 160

gac ata gat gag tgt cgt tac cgc tat tgc cag cat cga tgt gtg aac 585
Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn
165 170 175

ctg ccg ggc tct ttt cga tgc cag tgt gag cca ggc ttc cag ttg gga 633
Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly
180 185 190 195

cct aac aac cgc tct tgt gtg gat gtg aat gag tgt gac atg gga gcc 681
Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala
200 205 210

cca tgt gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc 729
Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg
215 220 225

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tgt aac cag ggc tat gag ctg cac cgg gat ggc ttc tcc tgc agc gat Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp	777
230 235 240	
atc gat gag tgc ggc tac tcc agt tac ctc tgc cag tac cgc tgt gtc Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val	825
245 250 255	
aac gag cca ggc cga ttc tcc tgt cac tgc cca caa ggc tac cag ctg Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu	873
260 265 270 275	
ctg gct aca agg ctc tgc caa gat att gac gag tgt gaa aca ggt gca Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Thr Gly Ala	921
280 285 290	
cac caa tgt tct gag gcc caa acc tgt gtc aac ttc cat ggg ggt tac His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr	969
295 300 305	
cgc tgt gtg gac acc aac cgt tgt gtg gag ccc tat gtc caa gtg tca Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val Gln Val Ser	1017
310 315 320	
gac aac cgc tgc ctc tgc cct gcc tcc aat ccc ctt tgt cga gag cag Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln	1065
325 330 335	
cct tca tcc att gtg cac cgc tac atg agc atc acc tca gag cga agt Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser Glu Arg Ser	1113
340 345 350 355	
gtg cct gct gac gtg ttt cag atc cag gca acc tct gtc tac cct ggt Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly	1161
360 365 370	
gcc tac aat gcc ttt cag atc cgt tct gga aac aca cag ggg gac ttc Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln Gly Asp Phe	1209
375 380 385	
tac att agg caa atc aac aat gtc agc gcc atg ctg gtc ctc gcc agg Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg	1257
390 395 400	
cca gtg acg gga ccc cgg gag tac gtg ctg gac ctg gag atg gtc acc Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr	1305
405 410 415	
atg aat tcc ctt atg agc tac cgg gcc agc tct gta ctg aga ctc acg Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr	1353
420 425 430 435	
gtc ttt gtg gga gcc tat acc ttc tgaagaccct caggggaaggg ccatgtgggg Val Phe Val Gly Ala Tyr Thr Phe	1407
440	
gcccccttccc cctcccatag cttaagcagc cccggggggcc tagggatgac cgttctgctt	1467
aaaggaacta tgatgtgaag gacaataaag ggagaaagaa ggaaaa	1513

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<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> MBP1 murine (complete sequence)

<400> 16

Met Leu Pro Phe Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
1 5 10 15

Phe Leu Leu Leu Leu Leu Gly Ala Ala Ser Pro Gln Asp Pro Glu Glu
20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Ala Asp
35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Ser Asp Leu His Gly Glu Gly Pro
85 90 95

Pro Pro Pro Ala Ala His Ala Gln Gln Pro Asn Pro Cys Pro Gln Gly
100 105 110

Tyr Glu Pro Asp Glu Gln Glu Ser Cys Val Asp Val Asp Glu Cys Thr
115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
165 170 175

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

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Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220

Leu Cys Arg Cys Asn Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Gly Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Thr Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Val
305 310 315 320

Gln Val Ser Asp Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Ser Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ser Gly Asn Thr Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

<210> 17

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<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 3' hMBP1

<400> 17

ctccgctccg aggtgatggt c

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide 5' hMBP1

<400> 18

tgtagctact ccagctacct c

21

<210> 19

<211> 1122

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 19

aagccagccg agccgccaga gccgcggggc gcgggggtgt cgcggggcca accccaggat 60

gctcccctgc gcctcctgcc taccgggtc tctactgctc tgggcgctgc tactgttgct 120

cttgggatca gcttctctc aggattctga agagcccgac agctacacgg aatgcacaga 180

tggctatgag tgggacccag acagccagca ctgccgggat gtcaacgagt gtctgaccat 240

ccctgaggcc tgcaaggggg aaatgaagt catcaaccac tacgggggct acttgtgcct 300

gccccgctcc gctgccgtca tcaacgacct acacggcgag ggacccccgc caccagtgcc 360

tcccgtcaa caccccaacc cctgcccacc aggctatgag cccgacgac aggacagctg 420

tgtggatgtg gacgagtgtg ccaggccct gcacgactgt cgccccagcc aggactgcca 480

taacttgcct ggctcctatc agtgcacctg ccctgatggt taccgcaaga tcgggcccga 540

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gtgtgtggac atagacgagt gccgctaccg ctactgccag caccgctgcg tgaacctgcc	600
tggctccttc cgctgccagt gcgagccggg cttccagctg gggcctaaca accgctcctg	660
tgttgatgtg aacgagtgtg acatgggggc cccatgcbag cagcgtgct tcaactccta	720
tgggaccttc ctgtgtcgct gccaccaggg ctatgagctg catcgggatg gcttctcctg	780
cagtgatatt gatgagtgtg gctactccag ctacctctgt cagtaccgct gcgtcaacga	840
gccaggccgt ttctcctgcc actgcccaca gggttaccag ctgctggcca cacgcctctg	900
ccaagacatt gatgagtgtg agtctggtgc gcaccagtgc tccgaggccc aaacctgtgt	960
caacttccat gggggctacc gctgcgtgga caccaaccgc tgcgtggagc cctacatcca	1020
ggctcttgag aaccgctgtc tctgcccggc ctccaaccct ctatgtcgag agcagccttc	1080
atccattgtg caccgctaca tgaccatcac ctcgagcgg ag	1122

<210> 20

<211> 684

<212> DNA

<213> Artificial sequence

<220>

<223> Human MBP1 cDNA (partial sequence)

<400> 20

tgtagctact ccagctacct ctgtcagtag cgctgcgtca acgagccagg ccgtttctcc	60
tgccactgcc cacaggggta ccagctgctg gccacacgcc tctgccaaga cattgatgag	120
tgtgagtctg gtgcgcacca gtgtccgag gcccaaacct gtgtcaactt ccatgggggc	180
taccgctgcb tggacaccaa ccgctgcgtg gagccctaca tccagggtctc tgagaaccgc	240
tgtctctgcc cggcctccaa cctctatgt cgagagcagc cttcatccat tgtgcaccgc	300
tacatgacca tcacctcgga gcgagcgtg cccgctgacg tgttccagat ccaggcgacc	360
tccgtctacc ccggtgccta caatgccttt cagatccgtg ctggaaactc gcagggggac	420
ttttacatta ggcaaatcaa caacgtcagc gccatgctgg tcctcgcccg gccggtgacg	480
ggcccccgag agtacgtgct ggacctggag atgggtacca tgaattccct catgagctac	540
cgggcccagct ctgtactgag gctcaccgtc tttgtagggg cctacacctt ctgaggagca	600
ggaggggagcc accctccctg cagctaccct agctgaggag cctgttgtga ggggcagaat	660
gagaaaggca ataaaggag aaag	684

<210> 21

<211> 1480

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<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<220>

<221> CDS

<222> (59)..(1387)

<400> 21

aagccagccg agccgccaga gccgcggggcc gcgggggtgt cgcgggccca accccagg	58
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1 5 10 15	
ctg cta ctg ttg ctc ttg gga tca gct tct cct cag gat tct gaa gag Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu	154
20 25 30	
ccc gac agc tac acg gaa tgc aca gat ggc tat gag tgg gac cca gac Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp	202
35 40 45	
agc cag cac tgc cgg gat gtc aac gag tgt ctg acc atc cct gag gcc Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala	250
50 55 60	
tgc aag ggg gaa atg aag tgc atc aac cac tac ggg ggc tac ttg tgc Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys	298
65 70 75 80	
ctg ccc cgc tcc gct gcc gtc atc aac gac cta cac ggc gag gga ccc Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro	346
85 90 95	
ccg cca cca gtg cct ccc gct caa cac ccc aac ccc tgc cca cca gcc Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly	394
100 105 110	
tat gag ccc gac gat cag gac agc tgt gtg gat gtg gac gag tgt gcc Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala	442
115 120 125	
cag gcc ctg cac gac tgt cgc ccc agc cag gac tgc cat aac ttg cct Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro	490
130 135 140	
ggc tcc tat cag tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro	538
145 150 155 160	
gag tgt gtg gac ata gac gag tgc cgc tac cgc tac tgc cag cac cgc Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg	586
165 170 175	
tgc gtg aac ctg cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe	634
180 185 190	
cag ctg ggg cct aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac	682

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Gln	Leu	Gly	Pro	Asn	Asn	Arg	Ser	Cys	Val	Asp	Val	Asn	Glu	Cys	Asp	
		195					200					205				
atg	ggg	gcc	cca	tgc	gag	cag	cgc	tgc	ttc	aac	tcc	tat	ggg	acc	ttc	730
Met	Gly	Ala	Pro	Cys	Glu	Gln	Arg	Cys	Phe	Asn	Ser	Tyr	Gly	Thr	Phe	
	210					215					220					
ctg	tgt	cgc	tgc	cac	cag	ggc	tat	gag	ctg	cat	cgg	gat	ggc	ttc	tcc	778
Leu	Cys	Arg	Cys	His	Gln	Gly	Tyr	Glu	Leu	His	Arg	Asp	Gly	Phe	Ser	
225					230					235					240	
tgc	agt	gat	att	gat	gag	tgt	agc	tac	tcc	agc	tac	ctc	tgt	cag	tac	826
Cys	Ser	Asp	Ile	Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	
				245					250					255		
cgc	tgc	gtc	aac	gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggc	874
Arg	Cys	Val	Asn	Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	
			260					265					270			
tac	cag	ctg	ctg	gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	922
Tyr	Gln	Leu	Leu	Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	
	275						280					285				
tct	ggc	gcg	cac	cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	970
Ser	Gly	Ala	His	Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	
	290					295					300					
ggg	ggc	tac	cgc	tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	1018
Gly	Gly	Tyr	Arg	Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	
305					310					315					320	
cag	gtc	tct	gag	aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	1066
Gln	Val	Ser	Glu	Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	
				325					330					335		
cga	gag	cag	cct	tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	1114
Arg	Glu	Gln	Pro	Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	
			340					345					350			
gag	cgg	agc	gtg	ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	1162
Glu	Arg	Ser	Val	Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	
		355					360					365				
tac	ccc	ggc	gcc	tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	1210
Tyr	Pro	Gly	Ala	Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	
	370					375					380					
ggg	gac	ttt	tac	att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	1258
Gly	Asp	Phe	Tyr	Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	
385					390					395				400		
ctc	gcc	cgg	ccg	gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	1306
Leu	Ala	Arg	Pro	Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	
				405					410					415		
atg	gtc	acc	atg	aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	1354
Met	Val	Thr	Met	Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	
			420					425					430			
agg	ctc	acc	gtc	ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag	gagggagcca				1407
Arg	Leu	Thr	Val	Phe	Val	Gly	Ala	Tyr	Thr	Phe						
		435				440										

Conseiller.ST25
 ccctccctgc agctacccta gctgaggagc ctgttgtag gggcagaatg agaaaggcaa 1467
 taaagggaga aag 1480

<210> 22

<211> 443

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 (complete sequence)

<400> 22

Met Leu Pro Cys Ala Ser Cys Leu Pro Gly Ser Leu Leu Leu Trp Ala
 1 5 10 15

Leu Leu Leu Leu Leu Leu Gly Ser Ala Ser Pro Gln Asp Ser Glu Glu
 20 25 30

Pro Asp Ser Tyr Thr Glu Cys Thr Asp Gly Tyr Glu Trp Asp Pro Asp
 35 40 45

Ser Gln His Cys Arg Asp Val Asn Glu Cys Leu Thr Ile Pro Glu Ala
 50 55 60

Cys Lys Gly Glu Met Lys Cys Ile Asn His Tyr Gly Gly Tyr Leu Cys
 65 70 75 80

Leu Pro Arg Ser Ala Ala Val Ile Asn Asp Leu His Gly Glu Gly Pro
 85 90 95

Pro Pro Pro Val Pro Pro Ala Gln His Pro Asn Pro Cys Pro Pro Gly
 100 105 110

Tyr Glu Pro Asp Asp Gln Asp Ser Cys Val Asp Val Asp Glu Cys Ala
 115 120 125

Gln Ala Leu His Asp Cys Arg Pro Ser Gln Asp Cys His Asn Leu Pro
 130 135 140

Gly Ser Tyr Gln Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro
 145 150 155 160

Glu Cys Val Asp Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg
 165 170 175

Conseiller.ST25

Cys Val Asn Leu Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe
180 185 190

Gln Leu Gly Pro Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp
195 200 205

Met Gly Ala Pro Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe
210 215 220

Leu Cys Arg Cys His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser
225 230 235 240

Cys Ser Asp Ile Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr
245 250 255

Arg Cys Val Asn Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly
260 265 270

Tyr Gln Leu Leu Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu
275 280 285

Ser Gly Ala His Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His
290 295 300

Gly Gly Tyr Arg Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile
305 310 315 320

Gln Val Ser Glu Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys
325 330 335

Arg Glu Gln Pro Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser
340 345 350

Glu Arg Ser Val Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val
355 360 365

Tyr Pro Gly Ala Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln
370 375 380

Gly Asp Phe Tyr Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val
385 390 395 400

Leu Ala Arg Pro Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu
405 410 415

Met Val Thr Met Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu
420 425 430

Conseiller.ST25

Arg Leu Thr Val Phe Val Gly Ala Tyr Thr Phe
435 440

<210> 23

<211> 817

<212> DNA

<213> Artificial Sequence

<220>

<223> Murine MBP1 cDNA (partial sequence)

<400> 23

gctgtggcag aaacccctga cttctgcca ccacctcca gcctcaggat gctccctttt	60
gcctcctgcc tccccgggtc tttgctgctc tgggcgtttc tgctgttgct cttgggagca	120
gcgtccccac aggatcccgga ggagccggac agctacacgg aatgcacaga tggctatgag	180
tgggatgcag acagccagca ctgccgggat gtcaacgagt gcctgaccat cccggaggct	240
tgcaaggggtg agatgaaatg catcaaccac tacggggggtt atttgtgtct gcctcgctct	300
gctgccgtca tcagtgatct ccatggtgaa ggacctccac cgccagcggc ccatgctcaa	360
caaccaaacc cttgcccgcg gggctacgag cctgatgaac aggagagctg tgtggatgtg	420
gacgagtgtg cccaggcttt gcatgactgt cgccctagtc aggactgcca taaccttcct	480
ggctcctacc agtgcacctg ccctgatggt taccgaaaaa ttggaccgga atgtgtggac	540
atagatgagt gtcgttaccg ctattgccag catcgatgtg tgaacctgcc gggctctttt	600
cgatgccagt gtgagccagg cttccagttg ggacctaa accgctcttg tgtggatgtg	660
aatgagtgtg acatgggagc cccatgtgag cagcgctgct tcaactccta tgggaccttc	720
ctgtgtcgct gtaaccaggg ctatgagctg caccgggatg gcttctcctg cagcgatatc	780
gatgagtgcg gctactccag ttacctctgc cagtacc	817

<210> 24

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-GAPDH oligonucleotide

<400> 24

cggagtcaac ggatttggtc gtat

24

Conseiller.ST25

<210> 25

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-GAPDH oligonucleotide

<400> 25

agccttctcc atggtggtga agac

24

<210> 26

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense-beta-actin oligonucleotide

<400> 26

cggttggcct tggggttcag ggggg

25

<210> 27

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-MBP1 oligonucleotide

<400> 27

gccctgatgg ttaccgcaag a

21

<210> 28

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> antisense MBP1 oligonucleotide

Conseiller.ST25

<400> 28
agcccccatg gaagttgaca c 21

<210> 29

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> sense-beta-actin oligonucleotide

<400> 29
gtggggcgcc ccaggcacca 20

<210> 30

<211> 1358

<212> DNA

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<220>

<221> CDS

<222> (1)..(885)

<400> 30
tgc acc tgc cct gat ggt tac cgc aag atc ggg ccc gag tgt gtg gac 48
Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
1 5 10 15

ata gac gag tgc cgc tac cgc tac tgc cag cac cgc tgc gtg aac ctg 96
Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
20 25 30

cct ggc tcc ttc cgc tgc cag tgc gag ccg ggc ttc cag ctg ggg cct 144
Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
35 40 45

aac aac cgc tcc tgt gtt gat gtg aac gag tgt gac atg ggg gcc cca 192
Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
50 55 60

tgc gag cag cgc tgc ttc aac tcc tat ggg acc ttc ctg tgt cgc tgc 240
Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
65 70 75 80

cac cag ggc tat gag ctg cat cgg gat ggc ttc tcc tgc agt gat att 288
His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
85 90 95

gat gag tgt agc tac tcc agc tac ctc tgt cag tac cgc tgc gtc aac 336

Conseiller.ST25

Asp	Glu	Cys	Ser	Tyr	Ser	Ser	Tyr	Leu	Cys	Gln	Tyr	Arg	Cys	Val	Asn									
			100					105					110											
gag	cca	ggc	cgt	ttc	tcc	tgc	cac	tgc	cca	cag	ggt	tac	cag	ctg	ctg	384								
Glu	Pro	Gly	Arg	Phe	Ser	Cys	His	Cys	Pro	Gln	Gly	Tyr	Gln	Leu	Leu									
		115					120					125												
gcc	aca	cgc	ctc	tgc	caa	gac	att	gat	gag	tgt	gag	tct	ggt	gcg	cac	432								
Ala	Thr	Arg	Leu	Cys	Gln	Asp	Ile	Asp	Glu	Cys	Glu	Ser	Gly	Ala	His									
	130					135					140													
cag	tgc	tcc	gag	gcc	caa	acc	tgt	gtc	aac	ttc	cat	ggg	ggc	tac	cgc	480								
Gln	Cys	Ser	Glu	Ala	Gln	Thr	Cys	Val	Asn	Phe	His	Gly	Gly	Tyr	Arg									
145					150					155					160									
tgc	gtg	gac	acc	aac	cgc	tgc	gtg	gag	ccc	tac	atc	cag	gtc	tct	gag	528								
Cys	Val	Asp	Thr	Asn	Arg	Cys	Val	Glu	Pro	Tyr	Ile	Gln	Val	Ser	Glu									
				165					170					175										
aac	cgc	tgt	ctc	tgc	ccg	gcc	tcc	aac	cct	cta	tgt	cga	gag	cag	cct	576								
Asn	Arg	Cys	Leu	Cys	Pro	Ala	Ser	Asn	Pro	Leu	Cys	Arg	Glu	Gln	Pro									
			180					185					190											
tca	tcc	att	gtg	cac	cgc	tac	atg	acc	atc	acc	tcg	gag	cgg	agc	gtg	624								
Ser	Ser	Ile	Val	His	Arg	Tyr	Met	Thr	Ile	Thr	Ser	Glu	Arg	Ser	Val									
		195					200					205												
ccc	gct	gac	gtg	ttc	cag	atc	cag	gcg	acc	tcc	gtc	tac	ccc	ggg	gcc	672								
Pro	Ala	Asp	Val	Phe	Gln	Ile	Gln	Ala	Thr	Ser	Val	Tyr	Pro	Gly	Ala									
	210					215					220													
tac	aat	gcc	ttt	cag	atc	cgt	gct	gga	aac	tcg	cag	ggg	gac	ttt	tac	720								
Tyr	Asn	Ala	Phe	Gln	Ile	Arg	Ala	Gly	Asn	Ser	Gln	Gly	Asp	Phe	Tyr									
225					230					235					240									
att	agg	caa	atc	aac	aac	gtc	agc	gcc	atg	ctg	gtc	ctc	gcc	cgg	ccg	768								
Ile	Arg	Gln	Ile	Asn	Asn	Val	Ser	Ala	Met	Leu	Val	Leu	Ala	Arg	Pro									
				245					250					255										
gtg	acg	ggc	ccc	cgg	gag	tac	gtg	ctg	gac	ctg	gag	atg	gtc	acc	atg	816								
Val	Thr	Gly	Pro	Arg	Glu	Tyr	Val	Leu	Asp	Leu	Glu	Met	Val	Thr	Met									
			260					265					270											
aat	tcc	ctc	atg	agc	tac	cgg	gcc	agc	tct	gta	ctg	agg	ctc	acc	gtc	864								
Asn	Ser	Leu	Met	Ser	Tyr	Arg	Ala	Ser	Ser	Val	Leu	Arg	Leu	Thr	Val									
		275					280					285												
ttt	gta	ggg	gcc	tac	acc	ttc	tgaggagcag gagggagcca ccctccctgc										915							
Phe	Val	Gly	Ala	Tyr	Thr	Phe																		
	290					295																		
agctacccta gctgaggagc ctgttgtag gggcagaatg agaaaggcaa taaagggaga																975								
aagaaagtcc tggtggctga ggtgggcggg tcacactgca ggaagcctca ggctggggca																1035								
gggtggcact tggggggggca ggccaagtgc acctaaatgg ggggtctctat atgttcaggc																1095								
ccagggggccc ccattgacag gagctgggag ctctgcacca cgagcttcag tcaccccag																1155								
aggagaggag gtaacgagga gggcggactc caggccccgg ccagagatt tggacttggc																1215								
tggcttgacg gggtcctaag aaactccact ctggacagcg ccaggaggcc ctgggttcca																1275								

Conseiller.ST25

ttcctaactc tgcctcaaac tgtacatttg gataagccct agtagttccc tgggcctgtt 1335
 tttctataaa acgaggcaac tgg 1358

<210> 31

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Human MBP1 C-term fragment

<400> 31

Cys Thr Cys Pro Asp Gly Tyr Arg Lys Ile Gly Pro Glu Cys Val Asp
 1 5 10 15

Ile Asp Glu Cys Arg Tyr Arg Tyr Cys Gln His Arg Cys Val Asn Leu
 20 25 30

Pro Gly Ser Phe Arg Cys Gln Cys Glu Pro Gly Phe Gln Leu Gly Pro
 35 40 45

Asn Asn Arg Ser Cys Val Asp Val Asn Glu Cys Asp Met Gly Ala Pro
 50 55 60

Cys Glu Gln Arg Cys Phe Asn Ser Tyr Gly Thr Phe Leu Cys Arg Cys
 65 70 75 80

His Gln Gly Tyr Glu Leu His Arg Asp Gly Phe Ser Cys Ser Asp Ile
 85 90 95

Asp Glu Cys Ser Tyr Ser Ser Tyr Leu Cys Gln Tyr Arg Cys Val Asn
 100 105 110

Glu Pro Gly Arg Phe Ser Cys His Cys Pro Gln Gly Tyr Gln Leu Leu
 115 120 125

Ala Thr Arg Leu Cys Gln Asp Ile Asp Glu Cys Glu Ser Gly Ala His
 130 135 140

Gln Cys Ser Glu Ala Gln Thr Cys Val Asn Phe His Gly Gly Tyr Arg
 145 150 155 160

Cys Val Asp Thr Asn Arg Cys Val Glu Pro Tyr Ile Gln Val Ser Glu
 165 170 175

Conseiller.ST25

Asn Arg Cys Leu Cys Pro Ala Ser Asn Pro Leu Cys Arg Glu Gln Pro
180 185 190

Ser Ser Ile Val His Arg Tyr Met Thr Ile Thr Ser Glu Arg Ser Val
195 200 205

Pro Ala Asp Val Phe Gln Ile Gln Ala Thr Ser Val Tyr Pro Gly Ala
210 215 220

Tyr Asn Ala Phe Gln Ile Arg Ala Gly Asn Ser Gln Gly Asp Phe Tyr
225 230 235 240

Ile Arg Gln Ile Asn Asn Val Ser Ala Met Leu Val Leu Ala Arg Pro
245 250 255

Val Thr Gly Pro Arg Glu Tyr Val Leu Asp Leu Glu Met Val Thr Met
260 265 270

Asn Ser Leu Met Ser Tyr Arg Ala Ser Ser Val Leu Arg Leu Thr Val
275 280 285

Phe Val Gly Ala Tyr Thr Phe
290 295

<210> 32

<211> 1663

<212> DNA

<213> Artificial Sequence

<220>

<223> murine fibulin 2 c-term fragment

<220>

<221> CDS

<222> (1)..(999)

<400> 32

gag ggc tct gaa tgt gtg gat gtg aat gag tgt gag aca ggt gtg cat	48
Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His	
1 5 10 15	

cgc tgt ggc gag ggc caa ctg tgc tat aac ctc cct gga tcc tac cgc	96
Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg	
20 25 30	

tgt gac tgc aag ccc ggc ttc cag agg gat gca ttc ggc agg act tgc	144
Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys	
35 40 45	

att gat gtg aac gaa tgc tgg gtc tcg ccg ggc cgc ctg tgc cag cac	192
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Conseiller.ST25																
Ile	Asp	Val	Asn	Glu	Cys	Trp	Val	Ser	Pro	Gly	Arg	Leu	Cys	Gln	His	
50						55					60					
aca	tgt	gag	aac	aca	ccg	ggc	tcc	tac	cgc	tgc	tcc	tgc	gct	gct	ggc	240
Thr	Cys	Glu	Asn	Thr	Pro	Gly	Ser	Tyr	Arg	Cys	Ser	Cys	Ala	Ala	Gly	
65					70					75					80	
ttc	ctt	ttg	gcc	gca	gat	ggc	aaa	cat	tgt	gaa	gat	gtg	aac	gag	tgc	288
Phe	Leu	Leu	Ala	Ala	Asp	Gly	Lys	His	Cys	Glu	Asp	Val	Asn	Glu	Cys	
				85					90					95		
gag	act	cgg	cgc	tgc	agc	cag	gaa	tgt	gcc	aac	atc	tat	ggc	tcc	tat	336
Glu	Thr	Arg	Arg	Cys	Ser	Gln	Glu	Cys	Ala	Asn	Ile	Tyr	Gly	Ser	Tyr	
			100					105					110			
cag	tgc	tac	tgc	cgt	cag	ggc	tac	cag	ctg	gca	gag	gat	ggg	cat	acc	384
Gln	Cys	Tyr	Cys	Arg	Gln	Gly	Tyr	Gln	Leu	Ala	Glu	Asp	Gly	His	Thr	
		115					120					125				
tgc	aca	gac	atc	gat	gag	tgt	gca	cag	ggc	gcg	ggc	att	ctc	tgt	acc	432
Cys	Thr	Asp	Ile	Asp	Glu	Cys	Ala	Gln	Gly	Ala	Gly	Ile	Leu	Cys	Thr	
	130					135					140					
ttc	cgc	tgt	gtc	aac	gtg	cct	ggg	agc	tac	cag	tgt	gca	tgc	cca	gag	480
Phe	Arg	Cys	Val	Asn	Val	Pro	Gly	Ser	Tyr	Gln	Cys	Ala	Cys	Pro	Glu	
145					150					155					160	
caa	ggg	tat	aca	atg	atg	gcc	aac	ggg	agg	tcc	tgc	aag	gac	ctg	gat	528
Gln	Gly	Tyr	Thr	Met	Met	Ala	Asn	Gly	Arg	Ser	Cys	Lys	Asp	Leu	Asp	
				165					170					175		
gag	tgt	gca	ctg	ggc	acc	cac	aac	tgc	tct	gag	gct	gag	acc	tgc	cac	576
Glu	Cys	Ala	Leu	Gly	Thr	His	Asn	Cys	Ser	Glu	Ala	Glu	Thr	Cys	His	
			180					185					190			
aat	atc	cag	ggg	agt	ttc	cgc	tgc	ctg	cgc	ttt	gat	tgt	cca	ccc	aac	624
Asn	Ile	Gln	Gly	Ser	Phe	Arg	Cys	Leu	Arg	Phe	Asp	Cys	Pro	Pro	Asn	
		195					200					205				
tat	gtc	cgt	gtc	tca	caa	acg	aag	tgc	gag	cgc	acc	aca	tgc	cag	gat	672
Tyr	Val	Arg	Val	Ser	Gln	Thr	Lys	Cys	Glu	Arg	Thr	Thr	Cys	Gln	Asp	
	210					215					220					
atc	acg	gaa	tgt	caa	acc	tca	cca	gct	cgc	atc	acg	cac	tac	cag	ctc	720
Ile	Thr	Glu	Cys	Gln	Thr	Ser	Pro	Ala	Arg	Ile	Thr	His	Tyr	Gln	Leu	
225					230					235					240	
aat	ttc	cag	aca	ggc	cta	ctg	gta	cct	gca	cat	atc	ttc	cgc	atc	ggc	768
Asn	Phe	Gln	Thr	Gly	Leu	Leu	Val	Pro	Ala	His	Ile	Phe	Arg	Ile	Gly	
				245					250					255		
cct	gct	ccc	gcc	ttt	gct	ggg	gac	acc	atc	tcc	ctg	acc	atc	acg	aag	816
Pro	Ala	Pro	Ala	Phe	Ala	Gly	Asp	Thr	Ile	Ser	Leu	Thr	Ile	Thr	Lys	
			260					265					270			
ggc	aat	gag	gag	ggc	tac	ttc	gtc	aca	cgc	aga	ctc	aat	gcc	tac	act	864
Gly	Asn	Glu	Glu	Gly	Tyr	Phe	Val	Thr	Arg	Arg	Leu	Asn	Ala	Tyr	Thr	
		275					280					285				
ggt	gtg	gta	tcc	ctg	cag	cgg	tct	gtt	ctg	gag	ccg	cgg	gac	ttt	gcc	912
Gly	Val	Val	Ser	Leu	Gln	Arg	Ser	Val	Leu	Glu	Pro	Arg	Asp	Phe	Ala	
	290					295					300					

Conseiller.ST25

cta gat gtg gag atg aag ctt tgg cgc cag ggc tct gtc act acc ttc 960
 Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
 305 310 315 320

ctg gcc aag atg tac atc ttc ttc acc act ttt gcc cca tgagggtgaca 1009
 Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro
 325 330

tgtcaggcaa tccctccagg tgatgcctgg gcggtgggca gctgcgccac tcctaagtgg 1069

ctttttgctg tgactctgta acttaactta atcatgctga gctgggttggc cttgagtctc 1129

taccctagag ggagggagat gcaccccagc aggcaactgag tacaggccag ggtcacccga 1189

ggctagatgg tgacctgcaa actggaaaca gccatagggg gcttctgaac tccactcctc 1249

aactatggct acagctgaca ttccattcct tcattccactg tgttcctcaa ttaaaaaaaaa 1309

aaatcagctg tgcattgtag cacagacctt taatcctagc actggggagg cagaggtagg 1369

tagatctctg agttccaggc cagcctgggtc tacactggga gttctaacca gccagagcta 1429

catagagaga ccctatctca acaaggaaaa aacgaaagaa atctctgtga gttccaggcc 1489

agcctgggtc acgctgggag ttctaaccag ccagagctac atagagagat cctatctcaa 1549

caaggaaaaa tgaaagaaat cattttaaaa ggtttttttt tttgctgttg ttgtttaatg 1609

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<210> 33

<211> 333

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine fibulin 2 c-term fragment

<400> 33

Glu Gly Ser Glu Cys Val Asp Val Asn Glu Cys Glu Thr Gly Val His
 1 5 10 15

Arg Cys Gly Glu Gly Gln Leu Cys Tyr Asn Leu Pro Gly Ser Tyr Arg
 20 25 30

Cys Asp Cys Lys Pro Gly Phe Gln Arg Asp Ala Phe Gly Arg Thr Cys
 35 40 45

Ile Asp Val Asn Glu Cys Trp Val Ser Pro Gly Arg Leu Cys Gln His
 50 55 60

Thr Cys Glu Asn Thr Pro Gly Ser Tyr Arg Cys Ser Cys Ala Ala Gly
 65 70 75 80

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Phe Leu Leu Ala Ala Asp Gly Lys His Cys Glu Asp Val Asn Glu Cys
85 90 95

Glu Thr Arg Arg Cys Ser Gln Glu Cys Ala Asn Ile Tyr Gly Ser Tyr
100 105 110

Gln Cys Tyr Cys Arg Gln Gly Tyr Gln Leu Ala Glu Asp Gly His Thr
115 120 125

Cys Thr Asp Ile Asp Glu Cys Ala Gln Gly Ala Gly Ile Leu Cys Thr
130 135 140

Phe Arg Cys Val Asn Val Pro Gly Ser Tyr Gln Cys Ala Cys Pro Glu
145 150 155 160

Gln Gly Tyr Thr Met Met Ala Asn Gly Arg Ser Cys Lys Asp Leu Asp
165 170 175

Glu Cys Ala Leu Gly Thr His Asn Cys Ser Glu Ala Glu Thr Cys His
180 185 190

Asn Ile Gln Gly Ser Phe Arg Cys Leu Arg Phe Asp Cys Pro Pro Asn
195 200 205

Tyr Val Arg Val Ser Gln Thr Lys Cys Glu Arg Thr Thr Cys Gln Asp
210 215 220

Ile Thr Glu Cys Gln Thr Ser Pro Ala Arg Ile Thr His Tyr Gln Leu
225 230 235 240

Asn Phe Gln Thr Gly Leu Leu Val Pro Ala His Ile Phe Arg Ile Gly
245 250 255

Pro Ala Pro Ala Phe Ala Gly Asp Thr Ile Ser Leu Thr Ile Thr Lys
260 265 270

Gly Asn Glu Glu Gly Tyr Phe Val Thr Arg Arg Leu Asn Ala Tyr Thr
275 280 285

Gly Val Val Ser Leu Gln Arg Ser Val Leu Glu Pro Arg Asp Phe Ala
290 295 300

Leu Asp Val Glu Met Lys Leu Trp Arg Gln Gly Ser Val Thr Thr Phe
305 310 315 320

Leu Ala Lys Met Tyr Ile Phe Phe Thr Thr Phe Ala Pro

325

Conseiller.ST25
330

<210> 34

<211> 16

<212> PRT

<213> Artificial Sequence

<220>

<223> Murine N-terminal signal sequence

<400> 34

Ala Val Ala Glu Thr Pro Asp Phe Cys Pro Pro Pro Pro Ser Leu Arg
1 5 10 15

<210> 35

<211> 19

<212> PRT

<213> Artificial Sequence

<220>

<223> Human N-terminal signal sequence

<400> 35

Ser Gln Pro Ser Arg Gln Ser Arg Gly Pro Arg Gly Cys Arg Gly Pro
1 5 10 15

Asn Pro Arg